

## SEQUENCE LISTING

<110> Wakamiya, N.  
<120> Novel Collectin  
<130> 19036/37157  
<150> JP HEI 10-237611  
<151> 1998-08-24  
<160> 32  
<210> 1  
<211> 2024  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (670)..(1695)

<400> 1  
gtcacgaatc tgcagcaaga taccagcgtg ctccagggca atctgcagaa ccaaattgtat 60  
tctcataatg tggatcatcat gaacctcaac aacctgaacc tgacctcaggt gcagcagagg 120  
aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc 180  
aagaacgact ttcaaaatct gcagcaggtt tttcttcaag ccaagaagga cagggtattgg 240  
ctgaaggaga aagtgcagag cttgcagacg ctggctgcca acaactctgc gttggccaaa 300  
gccaacaacg acaccctgga ggatatgaac agccagctca actcattcac aggtcagatg 360  
gagaacatca ccactatctc tcaagccaac gagcagaacc tgaaagacct gcaggactta 420  
cacaaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag 480  
ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg 540  
cggacgctga ccagcaatct aaatgaagtc aggaccactt gcacagatac ctttaccaaa 600  
cacacagatg atctgacctc cttgaataat accctggcca acatccgttt ggattctgtt 660  
tctctcagg atg caa caa gat ttg atg agg tcg agg tta gac act gaa gta 711  
Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val  
1 5 10  
gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag 759  
Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys  
15 20 25 30  
cat ggt cag ctc atc aag aat ttt aca ata cta caa ggt cca ccg ggc 807  
His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly  
35 40 45  
ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca 855  
Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro  
50 55 60  
act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct 903  
Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro  
65 70 75  
ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga 951  
Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly  
80 85 90  
gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc 999  
Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser  
95 100 105 110  
cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca 1047  
Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro  
115 120 125  
ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc 1095  
Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly  
130 135 140

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cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg 1143
Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val
145 150 155
cct gga cct cgg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca 1191
Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro
160 165 170
ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg 1239
Gly Pro Lys Gly Pro Gly Pro Gly Pro Gly Pro Ser Gly Ala Val Val
175 180 185 190
ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc 1287
Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly
195 200 205
tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca 1335
Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser
210 215 220
gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag 1383
Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys
225 230 235
tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata 1431
Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile
240 245 250
aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac 1479
Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp
255 260 265 270
tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac 1527
Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp
275 280 285
tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat 1575
Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His
290 295 300
ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac 1623
Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn
305 310 315
gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg 1671
Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg
320 325 330
gag aca gta ctg tca tct gca tta taacggactg tgatgggatac acatgagcaa 1725
Glu Thr Val Leu Ser Ser Ala Leu
335 340
atttttcagct ctcaaaggca aaggacactc cttttctaatt gcatcacctt ctcacagat 1785
tgaaaaaaaaaaa aaagcactg aaaaccaatt actgaaaaaa aattgacagc tagtggtttt 1845
taccatccgt cattacccaa agacttgga actaaaatgt tccccagggt gatagtctga 1905
ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965
atacaaatga tgtcttccaa agtatggaac actccaatca gaaaaagggt atcatcccg 2024

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&lt;210&gt; 2

&lt;211&gt; 547

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;223&gt; Deduced Amino Acid Sequence of Novel Collectin from Nucleotide Sequence

&lt;400&gt;2

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Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu
1 5 10 15
Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val
20 25 30
Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn
35 40 45
Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys
50 55 60

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[illegible]

<210> 3  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Modified Consensus Sequence of collectins Hybridizable with Novel Collectin

<400>3  
 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn  
           1                  5                  10                  15  
 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe  
                   20                  25

<210> 4  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Reverse Primer for Screening a Novel Collectin.

<400> 4  
 caatctgatg agaagtgat g 21

<210> 5  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Forward Primer for Screening a Novel Collectin.

<400> 5  
 acgaggggct ggatgggaca t 21

<210> 6  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence of three collectins which were reported heretofore

<400>6  
 Glu Asp Cys Val Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro  
           1                  5                  10                  15  
 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe  
                   20                  25

<210> 7  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> M13 Universal Primer Sequence for Sequencing

<400> 7  
 cgacgttgta aaacgacggc cagt 24

<210> 8  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> M13 Reverse Primer Sequence for Sequencing.

<400> 8  
 caggaaaca gctatgac 17

<210> 9  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a lambda gt11 Reverse Primer for Sequencing.

<400> 9  
 ttgacaccag accaactggt aatg 24

<210> 10  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a lambda gt11 Forward Primer for Sequencing.

<400> 10  
 ggtggcgacg actcctggag cccg 24

<210> 11  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Primer for Screening a Novel Collectin

<400>11  
 cgtgaaaatg aatggaagtg g 21

<210> 12  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Primer for Screening a Novel Collectin

<400>12  
 ttttatccat tgctgttcct c 21

<210> 13  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Primer for Sequencing a Novel Collectin

<400>13  
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 <210> 14  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Primer for Sequencing a Novel Collectin  
  
 <400>14  
 gctggtcccc ccgagagcg t 21  
  
 <210> 15  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a 1RC2 Primer for Cap Site Sequencing  
  
 <400> 15  
 caaggtacgc cacagcgat g 21  
  
 <210> 16  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Synthetic TGP1 Primer for Cap Site Sequencing  
  
 <400> 16  
 tcttcagttt ccctaattccc 20  
  
 <210> 17  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a 2RC2 Primer for Cap Site Sequencing  
  
 <400> 17  
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 <210> 18  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Synthetic TGP2 Primer for Cap Site Sequencing  
  
 <400> 18  
 cattcttgac aaacttcata g 21  
  
 <210> 19  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Primer for Screening a Novel Collectin  
  
 <400> 19  
 gaagacaagt cttcaactct tg 22  
  
 <210> 20  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Primer for Screening a Novel Collectin  
  
 <400> 20  
 ctctgagtct gtgaggccga tc 22  
  
 <210> 21  
 <211> 111  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Probe for Screening a Novel Collectin  
  
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 aaacagatgg tagggagaga gagccactgg atcggcctca cagactcaga g 111  
  
 <210> 22  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Forward Primer for Screening a Novel Collectin  
  
 <400> 22  
 gtgcccctgg ccctgcagaa tg 22  
  
 <210> 23  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Reverse Primer for Screening a Novel Collectin  
  
 <400> 23  
 gcatatcacc ctggggaaca ttttag 26  
  
 <210> 24  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Sequence of a Sense Primer for Screening Beta Actin  
  
 <400> 24  
 caagagatgg ccacggctgc t 21  
  
 <210> 25

<211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of an Antisense Primer for Screening Beta Actin

<400> 25  
 tcctttctgca tcctgtcggc a 21

<210> 26  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Sense Primer for Amplifying the Novel Collectin.

<400> 26  
 aaggaaaaaa gcggccgcat gcaacaagat ttgatgagg 39

<210> 27  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Reverse Primer for Amplifying the Novel Collectin

<400> 27  
 gctctagatt ataatgcaga tgacagtac 29

<210> 28  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 28  
 atgcaacaag atttgatgag g 21

<210> 29  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 29  
 cctacccggt agaattgacc 20

<210> 30  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> mannan-binding protein (MBP)



&lt;400&gt; 30

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala  
 1 5 10 15

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys  
 20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly  
 35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln  
 50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly  
 65 70 75 80

~~Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp~~  
 85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg  
 100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe  
 115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu  
 130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala  
 145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn  
 165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu  
 180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp  
 195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu  
 210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His  
 225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile  
 245

&lt;210&gt; 31

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; surfactant protein A (SP-A)

&lt;400&gt; 31

Met Trp Leu Cys Pro Leu Ala Leu Thr Leu Ile Leu Met Ala Ala Ser  
 1 5 10 15

Gly Ala Ala Cys Glu Val Lys Asp Val Cys Val Gly Ser Pro Gly Ile  
                   20                  25                  30  
 Pro Gly Thr Pro Gly Ser His Gly Leu Pro Gly Arg Asp Gly Arg Asp  
                   35                  40                  45  
 Gly Val Lys Gly Asp Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly  
                   50                  55                  60  
 Glu Thr Pro Cys Pro Pro Gly Asn Asn Gly Leu Pro Gly Ala Pro Gly  
                   65                  70                  75                  80  
 Val Pro Gly Glu Arg Gly Glu Lys Gly Glu Pro Gly Glu Arg Gly Pro  
                   85                  90                  95  
 Pro Gly Leu Pro Ala His Leu Asp Glu Glu Leu Gln Ala Thr Leu His  
                   100                  105                  110  
 Asp Phe Arg His Gln Ile Leu Gln Thr Arg Gly Ala Leu Ser Leu Gln  
                   115                  120                  125  
 Gly Ser Ile Met Thr Val Gly Glu Lys Val Phe Ser Ser Asn Gly Gln  
                   130                  135                  140  
 Ser Ile Thr Phe Asp Ala Ile Gln Glu Ala Cys Ala Arg Ala Gly Gly  
                   145                  150                  155                  160  
 Arg Ile Ala Val Pro Arg Asn Pro Glu Glu Asn Glu Ala Ile Ala Ser  
                   165                  170                  175  
 Phe Val Lys Lys Tyr Asn Thr Tyr Ala Tyr Val Gly Leu Thr Glu Gly  
                   180                  185                  190  
 Pro Ser Pro Gly Asp Phe Arg Tyr Ser Asp Gly Thr Pro Val Asn Tyr  
                   195                  200                  205  
 Thr Asn Trp Tyr Arg Gly Glu Pro Ala Gly Arg Gly Lys Glu Gln Cys  
                   210                  215                  220  
 Val Glu Met Tyr Thr Asp Gly Gln Trp Asn Asp Arg Asn Cys Leu Tyr  
                   225                  230                  235                  240  
 Ser Arg Leu Thr Ile Cys Glu Phe  
                   245

&lt;210&gt; 32

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; surfactant protein D (SP-D)

&lt;400&gt; 32

Met Leu Leu Phe Leu Leu Ser Ala Leu Val Leu Leu Thr Gln Pro Leu  
                   1                  5                  10                  15

Gly Tyr Leu Glu Ala Glu Met Lys Thr Tyr Ser His Arg Thr Thr Pro  
                   20                  25                  30

Ser Ala Cys Thr Leu Val Met Cys Ser Ser Val Glu Ser Gly Leu Pro  
                   35                  40                  45

Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Glu	Gly	Pro	Arg	Gly	Glu	Lys	Gly	50	55	60
Asp	Pro	Gly	Leu	Pro	Gly	Ala	Ala	Gly	Gln	Ala	Gly	Met	Pro	Gly	Gln	65	70	75
Ala	Gly	Pro	Val	Gly	Pro	Lys	Gly	Asp	Asn	Gly	Ser	Val	Gly	Glu	Pro	85	90	95
Gly	Pro	Lys	Gly	Asp	Thr	Gly	Pro	Ser	Gly	Pro	Pro	Gly	Pro	Pro	Gly	100	105	110
Val	Pro	Gly	Pro	Ala	Gly	Arg	Glu	Gly	Pro	Leu	Gly	Lys	Gln	Gly	Asn	115	120	125
Ile	Gly	Pro	Gln	Gly	Lys	Pro	Gly	Pro	Lys	Gly	Glu	Ala	Gly	Pro	Lys	130	135	140
Gly	Glu	Val	Gly	Ala	Pro	Gly	Met	Gln	Gly	Ser	Ala	Gly	Ala	Arg	Gly	145	150	155
Leu	Ala	Gly	Pro	Lys	Gly	Glu	Arg	Gly	Val	Pro	Gly	Glu	Arg	Gly	Val	165	170	175
Pro	Gly	Asn	Ala	Gly	Ala	Ala	Gly	Ser	Ala	Gly	Ala	Met	Gly	Pro	Gln	180	185	190
Gly	Ser	Pro	Gly	Ala	Arg	Gly	Pro	Pro	Gly	Leu	Lys	Gly	Asp	Lys	Gly	195	200	205
Ile	Pro	Gly	Asp	Lys	Gly	Ala	Lys	Gly	Glu	Ser	Gly	Leu	Pro	Asp	Val	210	215	220
Ala	Ser	Leu	Arg	Gln	Gln	Val	Glu	Ala	Leu	Gln	Gly	Gln	Val	Gln	His	225	230	235
Leu	Gln	Ala	Ala	Phe	Ser	Gln	Tyr	Lys	Lys	Val	Glu	Leu	Phe	Pro	Asn	245	250	255
Gly	Gln	Ser	Val	Gly	Glu	Lys	Ile	Phe	Lys	Thr	Ala	Gly	Phe	Val	Lys	260	265	270
Pro	Phe	Thr	Glu	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Ala	Gly	Gly	Gln	Leu	275	280	285
Ala	Ser	Pro	Arg	Ser	Ala	Ala	Glu	Asn	Ala	Ala	Leu	Gln	Gln	Leu	Val	290	295	300
Val	Ala	Lys	Asn	Glu	Ala	Ala	Phe	Leu	Ser	Met	Thr	Asp	Ser	Lys	Thr	305	310	315
Glu	Gly	Lys	Phe	Thr	Tyr	Pro	Thr	Gly	Glu	Ser	Leu	Val	Tyr	Ser	Asn	325	330	335
Trp	Ala	Pro	Gly	Glu	Pro	Asn	Asp	Asp	Gly	Gly	Ser	Glu	Asp	Cys	Val	340	345	350
Glu	Ile	Phe	Thr	Asn	Gly	Lys	Trp	Asn	Asp	Arg	Ala	Cys	Gly	Glu	Lys	355	360	365
Arg	Leu	Val	Val	Cys	Glu	Phe										370	375	